## Figure 1

```
  1  GATTCGGCACGAGAAACTTTTAAATCTTTAGTTATTTCTTAATACTTAGAACACTTAAAC    60


 61  AAAACTTTACAAAACAAAAGAGCAGAATAATTAGATCCTTTCAGGAGAATATGACTTTTT   120


121  TTTCCTAAGCACACTGGACCATAGAGGAAGACCAAAGGAATGTACAGTTGCCTGCTCCTT   180
  1                                                M  Y  S  C  L  L      7


181  CCTGACTTGCTGTATTTgACTCTGtCCCCACTGGTGGTGGCAATGCTATTAACCCCACAC   240
  8  P  D  L  L  Y  L  T  L  S  P  L  V  V  A  M  L  L  T  P  H     27


241  TTTAACGTGGCAAATCCCCAGAATCTGTTGGCTGGTCTCTGGCTAGAGAATGAGCACAGT   300
 28  F  N  V  A  N  P  Q  N  L  L  A  G  L  W  L  E  N  E  H  S     47


301  TTCACCCTTATGGCTCCAGAAAGAGCAAGAACACACCACTGCCAGCCAGAAGAGAGAAAA   360
 48  F  T  L  M  A  P  E  R  A  R  T  H  H  C  Q  P  E  E  R  K     67


361  GTCTTGTTCTGTCTCTTTCCCATTGTCCCAAATAGCCAAGCACAGGTTCAACCACCCCAA   420
 68  V  L  F  C  L  F  P  I  V  P  N  S  Q  A  Q  V  Q  P  P  Q     87


421  ATGCCACCCTTCTGCTGTGCAGCAGCCAAGGAAAAGACCCAGGAGGAGCAGCTCCAAGAA   480
 88  M  P  P  F  C  C  A  A  A  K  E  K  T  Q  E  E  Q  L  Q  E    107


481  CCTCTGGGCAGTCAGTGCCCAGATACTTGCCCCAATTCTTTGTGTCCAAGCCACACTCAG   540
108  P  L  G  S  Q  C  P  D  T  C  P  N  S  L  C  P  S  H  T  Q    127


541  CTGACAAAAGCCAACACTTTGTCTCTCTTTTTTTTTTTTCTTTTTTTTTGAGCAGAGTT   600
128  L  T  K  A  N  T  L  S  L  F  F  F  S  F  F  L  S  R  V    147


601  TCACTCTTGTCACCCAGGCTGGAGTGCAATGgCAGGATCTTGGCTCATTGCAACCTCCAC   660
148  S  L  L  S  P  R  L  E  C  N  G  R  I  L  A  H  C  N  L  H    167


661  CtCCCGGGTTCAAGCAATTCTCCTGTCTCAGCCTCTCGA   699
168  L  P  G  S  S  N  S  P  V  S  A  S  R      180
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# Figure 2

Figure 2